

**REMARKS/ARGUMENTS**

Applicants provisional elect Group 1; claims 1 to 26 on the basis of SEQ ID NO:1. Applicants provisionally elect BMP-2 as BMP species. These elections are made with traverse. It is believed that all of the present claims read on the elected species.

Traversal is based on the following grounds. Pending claim 1 is identical to claim 1 as amended under Article 19 PCT. The claim is directed to a polypeptide variant with increased heparin binding ability wherein the polypeptide variant is derived from a polypeptide being modified with a hexapeptide as identified in SEQ ID NO:1 or SEQ ID NO:2, wherein the polypeptide is a member of the DVR family including the TGF- $\beta$  super family.

The technical problem underlying the presently claimed invention may be considered to be the provision of DVR family member variants with increased heparin binding ability. The technical problem is solved by the provision of DVR family member variants being modified by hexapeptides as identified in SEQ ID NOS:1 or 2, wherein SEQ ID NOS:1 or 2 comprise at least two positively charged amino acid residues being capable of interacting with the negatively charged sulfated glucosaminoglycans.

The Examiner's position that there is no common structural feature linking together SEQ ID NOS:1 or 2 is submitted to be mistaken. Substituents X<sub>1</sub>, X<sub>4</sub> to X<sub>6</sub> of SEQ ID NOS:1 and 2 are identical. Thus, contrary to the Examiner's opinion, there is a common structural feature between both sequences.

The Examiner's position that there is no common functional feature between the two sequences, because referring to the IPER, allegedly sequences conferring increased heparin binding affinity are known, is also submitted to be mistaken. In the IPER, documents D1 to D5 have been cited. None of D1, D3 or D4 relates to the provision of polypeptide variants having an increased heparin binding ability. D2 and D5 do not disclose or suggest the particular pattern of at least two positively charged amino acid residues to increase the heparin binding affinity in accordance with the presently claimed invention. Therefore, there is also a common functional feature linking together the sequences SEQ ID NOS:1 and 2.

Appl. No. 09/913,467  
Amdt. dated July 1, 2004  
Reply to Office Action of June 1, 2004

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For these reasons, SEQ ID NOS:1 and 2 share a common structural and functional feature conferring distinction over the cited art. In view of the special technical feature shared by these sequences, it is respectfully submitted that restriction between them should not be required.

Further, the Examiner held that there is a lack of unity because the application contains claims directed to more than one species of the generic invention wherein allegedly the species BMP-2, BMP-4, BMP-6 to BMP-8 are not linked by a common technical feature in accordance with Rule 13.1 PCT.

However, the proteins are all members of the DVR (decapentalegic-Vg-related) family. None of the prior art documents discloses or suggests a DVR family member variant with increased heparin binding ability being modified with a hexapeptide as identified in SEQ ID NO:1 or 2. For these reasons, withdrawal of the election of species requirement is respectfully requested.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 650-326-2400.

Respectfully submitted,



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